RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/539, 032_

Source: _PCT_

Date Processed by STIC: _06/22/2005_

ENTERED

RAW SEQUENCE LISTING   DATE: 06/22/2005
PATENT APPLICATION: US/10/539,032   TIME: 10:30:27

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\06222005\J539032.raw

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   3 <110> APPLICANT: JAPAN SCIENCE AND TECHNOLOGY AGENCY
   5 <120> TITLE OF INVENTION: Glucose and/or fructose transporter 'NaGLT1' and gene
thereof
   7 <130> FILE REFERENCE: 4439-4034
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/539,032
C--> 10 <141> CURRENT FILING DATE: 2005-06-13
  12 <150> PRIOR APPLICATION NUMBER: JP P2002-363014
  13 <151> PRIOR FILING DATE: 2002-12-13
  15 <160> NUMBER OF SEQ ID NOS: 30
  17 <170> SOFTWARE: PatentIn Ver. 2.1
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 2173
  21 <212> TYPE: DNA
  22 <213> ORGANISM: Rattus norvegicus
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  25 <221> NAME/KEY: CDS
  26 <222> LOCATION: (111)..(1562)
  28 <400> SEQUENCE: 1
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  31 tggacctcac caaaaaccct ttgtctggag ccaccaagct ggggtcggaa atg gag     116
  32                                                            Met Glu
  33                                                             1
  35 ttc cgt ggg tcc ggg gcc act gct gtt gag cag cac ctc ctc cag tcc   164
  36 Phe Arg Gly Ser Gly Ala Thr Ala Val Glu Gln His Leu Leu Gln Ser
  37           5                   10                  15
  39 gag acc cca ggg aag aat ggg ctg cag gcc aca tcg agt gac caa gtg   212
  40 Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp Gln Val
  41          20                  25                  30
  43 gga aga aca ctg cgc tgg ttc acc act gtg gtt ctg aat gct gct ttc   260
  44 Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala Ala Phe
  45 35                  40                  45                  50
  47 ctg gga atg gga gtg agc gct gct gtg ctg gga ccc aca ttt cca gac   308
  48 Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe Pro Asp
  49                  55                  60                  65
  51 ctg gcc aga aac gtg aac cgg aac atc agc agc ctt tcc gaa atc ttc   356
  52 Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu Ile Phe
  53              70                  75                  80
  55 gtg ggc cga gcc ctc ggc tac ctg ggc ggc tct gtg gtt ggt ggg gtg   404
  56 Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly Gly Val
  57              85                  90                  95
  59 ctt ttc gac tgc atg aat cat ttt cta ctt ttg ggg ctg tcc cac ctg   452
  60 Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser His Leu
  61          100                 105                 110
  63 ctt act gcg gcc ggt ctt tac ctc act cct ttc tgt aaa aca gct gcc   500
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 64 Leu Thr Ala Ala Gly Leu Tyr Leu Thr Pro Phe Cys Lys Thr Ala Ala
 65 115                 120                 125                 130
 67 tta ctg act gcc atg atg tct att acc ggt gtc tca ttt ggt gtt ctg    548
 68 Leu Leu Thr Ala Met Met Ser Ile Thr Gly Val Ser Phe Gly Val Leu
 69                 135                 140                 145
 71 gat aca ggt ggg aat gtc ctc atc ttg gac.ctt tgg ggg gac aaa gga    596
 72 Asp Thr Gly Gly Asn Val Leu Ile Leu Asp Leu Trp Gly Asp Lys Gly
 73                 150                 155                 160
 75 gcc cca cat att cag gcc ttg cac ttc agt ttc gcc ttg ggt gcc ttc    644
 76 Ala Pro His Ile Gln Ala Leu His Phe Ser Phe Ala Leu Gly Ala Phe
 77             165                 170                 175
 79 ctg gct ccc ctg ctg gct aaa ttg gcc tgg ggt acc aca gca tct gct    692
 80 Leu Ala Pro Leu Leu Ala Lys Leu Ala Trp Gly Thr Thr Ala Ser Ala
 81     180                 185                 190
 83 cag aac cac aca gag cct cag tta gac cgt tca gcc ttg aac cga tcc    740
 84 Gln Asn His Thr Glu Pro Gln Leu Asp Arg Ser Ala Leu Asn Arg Ser
 85 195                 200                 205                 210
 87 ttt gaa gcc gcc tca gac tct gtg ttg gcg gta cct gac gac atg aat    788
 88 Phe Glu Ala Ala Ser Asp Ser Val Leu Ala Val Pro Asp Asp Met Asn
 89             215                 220                 225
 91 ctt ctg tgg gcg tac gct tcc att gga acc tat gtt cta gta ctt tct    836
 92 Leu Leu Trp Ala Tyr Ala Ser Ile Gly Thr Tyr Val Leu Val Leu Ser
 93             230                 235                 240
 95 gtc ttc ctg ttt gct cca ttc ttt aaa aag agg tca aag cag aaa aaa    884
 96 Val Phe Leu Phe Ala Pro Phe Phe Lys Lys Arg Ser Lys Gln Lys Lys
 97             245                 250                 255
 99 tcc gca gcg tct gct cag gga gct cga agg gct aaa tac cac agg gcc    932
100 Ser Ala Ala Ser Ala Gln Gly Ala Arg Arg Ala Lys Tyr His Arg Ala
101     260                 265                 270
103 ctg cta tgc ctc ctc ttc ctc ttc ttc ttc ttc tac gtg gga gcg gag    980
104 Leu Leu Cys Leu Leu Phe Leu Phe Phe Phe Phe Tyr Val Gly Ala Glu
105 275                 280                 285                 290
107 gtg acc tac ggc tct tac gta ttc tcc ttc gcc acc acc cac gtt ggc   1028
108 Val Thr Tyr Gly Ser Tyr Val Phe Ser Phe Ala Thr Thr His Val Gly
109                 295                 300                 305
111 atg gaa gag agc gag gca gct ggc ttg aac tcc atc ttc tgg ggg acc   1076
112 Met Glu Glu Ser Glu Ala Ala Gly Leu Asn Ser Ile Phe Trp Gly Thr
113             310                 315                 320
115 ttc gca gcc tgc agg ggc ctg gcc atc ttc ttc gca acg ctc tta cag   1124
116 Phe Ala Ala Cys Arg Gly Leu Ala Ile Phe Phe Ala Thr Leu Leu Gln
117             325                 330                 335
119 cct ggg acc atg atg gtg ttg tgt aac att ggc agc ctg gcc tca tct   1172
120 Pro Gly Thr Met Met Val Leu Cys Asn Ile Gly Ser Leu Ala Ser Ser
121     340                 345                 350
123 ttc ttt ctg gtg ctt ttt gac aag agc cct ctt tgc ctc tgg atc gcg   1220
124 Phe Phe Leu Val Leu Phe Asp Lys Ser Pro Leu Cys Leu Trp Ile Ala
125 355                 360                 365                 370
127 tct tct gtg tat gga gcc tca atg gct gcc acg ttt ccc agc ggc atc   1268
128 Ser Ser Val Tyr Gly Ala Ser Met Ala Ala Thr Phe Pro Ser Gly Ile
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129                  375                 380                 385
131 tcc tgg att gag cag tac acc acc tta act ggg aaa tcc gct gcg ttc   1316
132 Ser Trp Ile Glu Gln Tyr Thr Thr Leu Thr Gly Lys Ser Ala Ala Phe
133                  390                 395                 400
135 att ctg gtt ggt gct gcc ctg gga cta atg gcg act cct gca tta tct   1364
136 Ile Leu Val Gly Ala Ala Leu Gly Leu Met Ala Thr Pro Ala Leu Ser
137          405                 410                 415
139 gga att ctt cag gga cac tat ccc gat ctg cca gta att ctg tac atg   1412
140 Gly Ile Leu Gln Gly His Tyr Pro Asp Leu Pro Val Ile Leu Tyr Met
141       420                 425                 430
143 tgt ctg ggc tca gca gta tta aca act gtg tta ttc cct gtg atg tat   1460
144 Cys Leu Gly Ser Ala Val Leu Thr Thr Val Leu Phe Pro Val Met Tyr
145 435                 440                 445                 450
147 aaa gta gcc acc tta cct ctg gat cga aag cag gaa aaa agc atc aac   1508
148 Lys Val Ala Thr Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser Ile Asn
149                  455                 460                 465
151 agt gag ggc cag aaa ata tta ctt tct agc tct agg cta atc aag gaa   1556
152 Ser Glu Gly Gln Lys Ile Leu Leu Ser Ser Ser Arg Leu Ile Lys Glu
153                  470                 475                 480
155 gct aaa tgaaagagga aggggaaagg tgtgaaagca cgtgcgcgcg tgtgtgcgca   1612
156 Ala Lys
158 tgcacgcgca cgcgtaatgg ttttgcggtg gttaaatgaa agaatgggac attctctaat 1672
160 aaaaatacaa tagaaatgcc tttatataac ccatagctga ggtctctaag caactctcct 1732
162 gaaatattct gcagccaggg tcttctccag ctgacaggga gcacgcagtc atgaggcacc 1792
164 aggtctcctg agaccccctta cactgccctc attgaagtta tctctcagcc catgattcta 1852
166 ggaaagaaaa gtatttctaa aataaaatcc acgacttcca gagatcctgt aagacagctc 1912
168 tgagagatca atgtaactgc cagcaccttc ttcatttcca tgaagtgaga cacagaacag 1972
170 aaatagtttt aaacgtatgc tcctggggct ggtgagatgg cttagtggtt aagagcactg 2032
172 actgctcttc caaaggtcct gagttcaaat cccagcaacc acatggtggc tcacaactat 2092
174 ctgtaatgag atctgatgcc ttcttctggt gtgtctgaag acagcgacag tgtactcata 2152
176 tacatcaaat aaataatatt t                                           2173
179 <210> SEQ ID NO: 2
180 <211> LENGTH: 484
181 <212> TYPE: PRT
182 <213> ORGANISM: Rattus norvegicus
184 <400> SEQUENCE: 2
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188 Gln Ser Glu Thr Pro Gly Lys Asn Gly Leu Gln Ala Thr Ser Ser Asp
189                  20                  25                  30
191 Gln Val Gly Arg Thr Leu Arg Trp Phe Thr Thr Val Val Leu Asn Ala
192          35                  40                  45
194 Ala Phe Leu Gly Met Gly Val Ser Ala Ala Val Leu Gly Pro Thr Phe
195       50                  55                  60
197 Pro Asp Leu Ala Arg Asn Val Asn Arg Asn Ile Ser Ser Leu Ser Glu
198 65                  70                  75                  80
200 Ile Phe Val Gly Arg Ala Leu Gly Tyr Leu Gly Gly Ser Val Val Gly
201                  85                  90                  95
203 Gly Val Leu Phe Asp Cys Met Asn His Phe Leu Leu Leu Gly Leu Ser
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204              100              105              110
206 His Leu Leu Thr Ala Ala Gly Leu Tyr Leu Thr Pro Phe Cys Lys Thr
207         115              120              125
209 Ala Ala Leu Leu Thr Ala Met Met Ser Ile Thr Gly Val Ser Phe Gly
210     130              135              140
212 Val Leu Asp Thr Gly Gly Asn Val Leu Ile Leu Asp Leu Trp Gly Asp
213 145              150              155              160
215 Lys Gly Ala Pro His Ile Gln Ala Leu His Phe Ser Phe Ala Leu Gly
216             165              170              175
218 Ala Phe Leu Ala Pro Leu Leu Ala Lys Leu Ala Trp Gly Thr Thr Ala
219         180              185              190
221 Ser Ala Gln Asn His Thr Glu Pro Gln Leu Asp Arg Ser Ala Leu Asn
222     195              200              205
224 Arg Ser Phe Glu Ala Ala Ser Asp Ser Val Leu Ala Val Pro Asp Asp
225     210              215              220
227 Met Asn Leu Leu Trp Ala Tyr Ala Ser Ile Gly Thr Tyr Val Leu Val
228 225              230              235              240
230 Leu Ser Val Phe Leu Phe Ala Pro Phe Phe Lys Lys Arg Ser Lys Gln
231             245              250              255
233 Lys Lys Ser Ala Ala Ser Ala Gln Gly Ala Arg Arg Ala Lys Tyr His
234         260              265              270
236 Arg Ala Leu Leu Cys Leu Leu Phe Leu Phe Phe Phe Tyr Val Gly
237         275              280              285
239 Ala Glu Val Thr Tyr Gly Ser Tyr Val Phe Ser Phe Ala Thr Thr His
240     290              295              300
242 Val Gly Met Glu Glu Ser Glu Ala Ala Gly Leu Asn Ser Ile Phe Trp
243 305              310              315              320
245 Gly Thr Phe Ala Ala Cys Arg Gly Leu Ala Ile Phe Phe Ala Thr Leu
246             325              330              335
248 Leu Gln Pro Gly Thr Met Met Val Leu Cys Asn Ile Gly Ser Leu Ala
249         340              345              350
251 Ser Ser Phe Phe Leu Val Leu Phe Asp Lys Ser Pro Leu Cys Leu Trp
252     355              360              365
254 Ile Ala Ser Ser Val Tyr Gly Ala Ser Met Ala Ala Thr Phe Pro Ser
255     370              375              380
257 Gly Ile Ser Trp Ile Glu Gln Tyr Thr Thr Leu Thr Gly Lys Ser Ala
258 385              390              395              400
260 Ala Phe Ile Leu Val Gly Ala Ala Leu Gly Leu Met Ala Thr Pro Ala
261             405              410              415
263 Leu Ser Gly Ile Leu Gln Gly His Tyr Pro Asp Leu Pro Val Ile Leu
264         420              425              430
266 Tyr Met Cys Leu Gly Ser Ala Val Leu Thr Thr Val Leu Phe Pro Val
267         435              440              445
269 Met Tyr Lys Val Ala Thr Leu Pro Leu Asp Arg Lys Gln Glu Lys Ser
270     450              455              460
272 Ile Asn Ser Glu Gly Gln Lys Ile Leu Leu Ser Ser Ser Arg Leu Ile
273 465              470              475              480
275 Lys Glu Ala Lys
279 <210> SEQ ID NO: 3
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RAW SEQUENCE LISTING   DATE: 06/22/2005
PATENT APPLICATION: US/10/539,032   TIME: 10:30:27

Input Set : A:\Sequence Listing.txt
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280 <211> LENGTH: 20
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-1 forward
286       primer
288 <400> SEQUENCE: 3
289 tcggaaatgg agttccgtgg                                          20
292 <210> SEQ ID NO: 4
293 <211> LENGTH: 22
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-2 forward
299       primer
301 <400> SEQUENCE: 4
302 agctgcctta ctgactgcca tg                                       22
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 21
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-3 forward
312       primer
314 <400> SEQUENCE: 5
315 tacgtattct ccttcgccac c                                        21
318 <210> SEQ ID NO: 6
319 <211> LENGTH: 21
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-4 forward
325       primer
327 <400> SEQUENCE: 6
328 tgtgtaacat tggcagcctg g                                        21
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 20
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence:T3-5 forward
338       primer
340 <400> SEQUENCE: 7
341 taacccatag ctgaggtctc                                          20
344 <210> SEQ ID NO: 8
345 <211> LENGTH: 24
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
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VERIFICATION SUMMARY   DATE: 06/22/2005
PATENT APPLICATION: US/10/539,032   TIME: 10:30:28

Input Set : **A:\Sequence Listing.txt**
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date